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Genetic parameters and predictions for direct and maternal growth traits in a multibreed Angus–Brahman cattle population using genomic–polygenic and polygenic models

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ABSTRACT

The objectives of this research were to compare variance components, genetic parameters, and EBV rankings for birth weight (BW) direct and maternal, weaning weight (WW) direct and maternal, and postweaning gain from 205 d to 365 d (PWG) direct using three genomic–polygenic and one polygenic model representing four plausible beef cattle genetic evaluation scenarios for growth traits under subtropical conditions in the US southern region. In addition, EBV trends as percentage Brahman increased from 0% to 100% were evaluated for each trait and model. The dataset included 5264 animals from a multibreed Angus–Brahman population born from 1987 to 2013. Genomic–polygenic models 1 (GP1; pedigree relationships for all animals; genomic relationships for genotyped animals), 2 (GP2; pedigree relationships for non-genotyped animals; genomic relationships for genotyped animals), and 3 (GP3; no pedigree relationships; genomic relationships for genotyped animals) used actual and imputed genotypes from 46,768 SNP markers. Variance components and genetic parameters were estimated using REML procedures. Variance component and genetic parameter estimates from GP1 were the most similar to those from the polygenic model, followed by those from GP2, and the least similar (especially for maternal traits) were those from GP3. Similarly, the highest rank correlations were those between animal EBV from the polygenic model and GP1, followed by those between animal EBV from GP1 and GP2 and between the polygenic model and GP2. Model GP3 performed poorly for maternal traits due to ignoring calf–dam relationships. These results indicated that the polygenic model and genomic–polygenic model 1 should be preferred. However, high genotyping costs still make the polygenic model preferable for commercial beef cattle operations. Brahman animals tended to have higher EBV for BW direct and WW direct, and lower EBV for PWG direct, BW maternal, and WW maternal. However, low regression coefficients for EBV on Brahman fraction ensured that high, medium, and low EBV animals from all breed compositions existed in this multibreed population.

1. Introduction

Utilization of genotype information for genetic evaluation of cattle has become widespread in beef and dairy cattle. Genomic evaluations are currently routinely conducted in dairy cattle in the US and other countries (VanRaden, 2008; Harris and Johnson, 2010; VanRaden et al., 2011, 2013; Legarra and Ducrocq, 2012). Conversely, the US beef industry has only recently begun to implement national genomic evaluations that combine phenotypic, pedigree, and genotypic information (Fernando and Garrick, 2013). Purebred breeders and commercial cattle producers have been encouraged by breed associations and private companies to genotype their animals with one or more chips of various densities. Genotyping animals from purebred cattle operations that submit phenotypes, pedigree, and genotypes to breed associations conducting national genetic evaluations will likely enhance the ability of individual cattle breeders to identify superior animals. However, the potential usefulness of genotyping to enhance genetic selection within commercial cattle operations that do in-house genetic evaluations seems less clear. Increases in prediction

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accuracies will depend on the extent of genotyping (and density of genotyping chips), the availability of individual phenotypes, and the completeness of pedigree information.

Implementation of genomic evaluation methodology has been greatly facilitated by the development of the single-step genomic evaluation procedure (Aguilar et al., 2010). The integration of the unified procedure into the freely available BLUPF90 family of programs has increased the feasibility of utilizing of genomic procedures to analyze traits that are not only affected by direct genetic effects, but also by maternal effects such as preweaning weights in beef cattle. Estimates of genetic parameters, prediction accuracies, and animal rankings for these types of traits using genomic and polygenic models have yet to be evaluated. Further, considering the multibreed nature of the current beef cattle national genetic evaluation system in the US, genomic and polygenic models for growth traits need to be compared using information from multibreed populations. The only reported work on this subject was a comparison of various genomic evaluation models using simulated weaning direct and maternal QTL effects (Lourenco et al., 2013).

This research was aimed at comparing multibreed beef cattle evaluations for growth traits using four scenarios defined in terms of availability of phenotypic, pedigree, and genotypic information to represent genetic evaluations in purebred and in commercial cattle herds. The four scenarios represented genetic evaluations using: 1) all available phenotypic, pedigree, and genotypic data (genomic–polygenic model 1; 2) all available phenotypic data, pedigree from non-genotyped animals only, and all available genotypic data (genomic–polygenic model 2); and 2) all available phenotypic and genotypic data, but no pedigree information (genomic–polygenic model 3); and 4) all available phenotypic and pedigree data and no genotypic information (polygenic model). Scenarios 1 and 4 represent purebred cattle breeders and commercial producers that keep all feasible records and scenarios 2 and 3 represent two cases of commercial operations with incomplete information. These four scenarios were constructed using information from the multibreed Angus–Brahman population of the University of Florida. The diallel-mating design of this population has created a continuum of breed compositions ranging from 100% Angus to 100% Brahman over its 26 years of existence (1987–2013). Most beef cattle in the southern region of the US, and Florida in particular, span the range from completely Brahman to completely *Bos taurus*, where Angus is the most represented *B. taurus* breed. This makes the multibreed Angus–Brahman population of the University of Florida well-suited to study these four scenarios under the subtropical conditions of the US southern region. Thus, the objectives of this research were: 1) to compare variance components and genetic parameters (heritabilities, genetic correlations) for birth weight direct and maternal, weaning weight direct and maternal, and postweaning gain direct computed under scenarios 1, 2, 3, and 4; 2) to compare rankings of animals for birth weight direct and maternal, weaning weight direct and maternal, and postweaning gain direct across scenarios 1, 2, 3, and 4; and 3) to evaluate EBV trends for each trait computed in scenarios 1, 2, 3, and 4 as percentage Brahman increased from 0% to 100% in a multibreed Angus–Brahman population under subtropical environmental conditions.

2. Materials and methods

2.1. Animals and traits

The University of Florida Institutional Animal Care and Use Committee approved the research protocol for animals involved in this project (IACUC Protocol number 201003744). Animals used in this research belonged to the long-term multibreed Angus–Brahman (MAB) project of the University of Florida, Gainesville. The mating plan in the MAB herd followed a diallel design where sires from six breed groups were mated to dams of these same breed groups (Elzo and Wakeman, 1998). The mating breed groups were defined in terms of ranges of Angus (A) and Brahman (B) percentages as follows: 1) BG1 = 100% A to (80% A 20% B); 2) BG2 = (60% A 40% B) to (79% A 21% B); 3) BG3 = Brangus = (62.5% A 37.5% B); 4) BG4 = (40% A 60% B) to (59% A 41% B); 5) BG5 = (20% A 80% B) to (39% A 61%B); and 6) BG6 = (19% A 81% B) to 100% B. The dataset included information on preweaning and postweaning growth from calves born between 1987 and 2013. There were 5264 calves with birth weights (BW, kg; 2689 bulls and 2575 heifers), 5262 calves with weaning weights adjusted to 205 d of age (WW, kg; 614 bulls, 2573 heifers, and 2075 steers), and 3846 calves with postweaning gains from 205 d to 365 d of age (PWG, kg; 209 bulls, 1784 heifers, and 1853 steers). These calves were the progeny of 293 sires (54 BG1, 37 BG2, 60 BG3, 35 BG4, 38 BG5, and 69 BG6) and 1725 dams (291 BG1, 249 BG2, 254 BG3, 349 BG4, 200 BG5, and 282 BG6). Number of calves per breed group, means, and SD for BW, WW, and PWG are presented in Table 1. Except for two, all calves with BW had WW records, and 73% of calves with WW information had PWG data. Culling and sale of excess calf inventory at weaning were responsible for the lower number of animals with postweaning gain phenotypes.

2.2. Feeding and management

Calves stayed at the Pine Acres Research Station (1987–1994) and at the Beef Research Unit (1995–2013) of the University of Florida from birth (December to March) to weaning (August, September). Preweaning, cows and calves were kept in bahiagrass pastures (*Paspalum notatum*) with access to a complete mineral supplement (UF University Special Hi–Cu Mineral, University of Florida, Animal Science Department, Gainesville, Florida). They also received a supplement of bermudagrass (*Cynodon dactylon*) hay and cotton seed (*Gossypium spp.*) meal during winter (mid-December to mid-March). Postweaning, calves were kept at their birth location (Pine Acres Research Station and at the Beef Research Unit), except from 2006 to 2010 when they were kept at the University of Florida Feed Efficiency Facility (UFFEF). When calves remained at their respective birth locations (1987–2005 and 2011–2013), they were kept in bahiagrass pastures supplemented with bahiagrass hay, concentrate (1.6–3.6 kg per day; 14.0% CP; 488 Pellet Medicated Weaning Ration, Lakeland Animal Nutrition, Lakeland, Florida; soy hull pellets), and free access to mineral

Table 1
Numbers of calves, means and standard deviations per breed group and total.

Breed group[b]	Trait[a]								
	BW (kg)			WW (kg)			PWG (kg)		
	N	Mean	SD	*N*	Mean	SD	*N*	Mean	SD
BG1	764	31.6	5.6	764	210.5	32.5	576	75.2	62.7
BG2	792	31.9	5.5	792	221.1	30.6	625	83.1	61.2
BG3	730	33.7	6.1	728	217.2	33.3	531	83.1	62.5
BG4	1338	33.8	6.4	1338	223.8	29.1	944	79.9	58.9
BG5	722	34.6	6.4	722	221.3	31.5	574	71.4	54.2
BG6	918	33.7	6.1	918	207.6	30.5	596	72.3	53.0
Total	5264	33.3	6.1	5262	217.4	31.6	3846	77.7	59.0

[a] BW = birth weight; WW = weaning weight adjusted to 205 d of age; PWG = postweaning gain from 205 d to 365 d of age.

[b] Breed group: BG1 = 100% A to (80% A 20% B); 2) BG2 = (60% A 40% B) to (79% A 21% B); 3) BG3 = Brangus = (62.5% A 37.5% B); 4) BG4 = (40% A 60% B) to (59% A 41% B); 5) BG5 = (20% A 80% B) to (39% A 61%B); and 6) BG6 = (19% A 81% B) to 100% B; A = Angus, B = Brahman.